P3933

Machine learning for antibiotic optimisation in multi-morbid patients

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Why?

- **Co-morbidities** defined here as chronic long-term medical conditions are a **major challenge in healthcare**[1]
- **Challenges exist** with representing and using co-morbidity data in AI systems[1]:
  - **Combinatorial complexity** due to the large number of unique diseases
  - Sparsity, missingness and a **lack of data** particularly for those with rare diseases or complex co-morbidity combinations
  - **Heterogeneity** in how chronic conditions are recorded
- Existing AI research on co-morbid patients does not tackle these problems and therefore **lacks appropriate representation**

Aim

Creating **meaningful embeddings** from **external medically grounded knowledge**, to help **overcome such challenges** and **support downstream AI applications**

How?

- Processed **SNOMED CT**[2] a comprehensive clinical healthcare terminology into a connected undirected graph
- Generated **disease embeddings** through Node2vec[3] with optimization to reduce the mean SNOMED distance (shortest path length) between each node and their nearest neighbor
- Tested disease embeddings as sole features to **supervised learning models** for clinically relevant predictions
- Defined **co-morbid patient embeddings** as the mean of all the SNOMED disease embeddings for a particular individual
- Evaluated co-morbid patient embeddings through a **task to retrieve the most similar patient** for any given unique co-morbid patient, where no identical match was possible
  - Retrieved similar patients in our method through **nearest neighbor lookup** based on euclidian distance
  - Utilized two **novel metrics** and **human experts** as evaluators
- Tested similar patients' methodology on an **antibiotic treatment prediction task**

Results

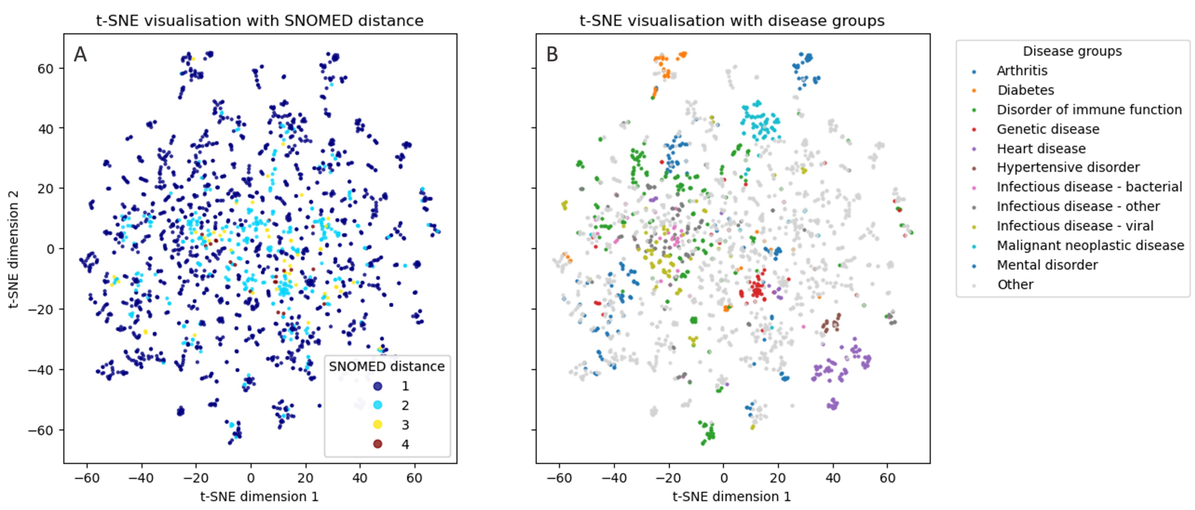

Figure 1: t-SNE visualisations of the SNOMED disease embeddings (2,133 diseases) with [A] nearest neighbor SNOMED distance (hyperparameter optimisation resulted in a mean of 1.23) and [B] high-level disease groups displayed.

Table 1: Mean unseen test set AUROC results for supervised learning classification tasks in different populations.

		Year Mortality		Long length of stay	
Features	Model	Overall	Rarest co-morbidities	Overall	Rarest co-morbidities
Charlson co-moribdity categories	Logistic regression	0.65 (SD 0.01)	0.50 (SD <0.01)	0.60 (SD 0.01)	0.50 (SD 0.03)
One hot encodings	Logistic regression	0.79 (SD 0.02)	0.80 (SD 0.23)	0.72 (SD 0.01)	0.55 (SD 0.11)
Random SNOMED disease embeddings	Set transformer	0.80 (SD 0.03)	0.56 (SD 0.33)	0.74(SD 0.02)	0.52 (SD 0.23)
SNOMED disease embeddings	Set transformer	**0.82 (SD 0.02)**	**0.85 (SD 0.14)**	**0.75 (SD 0.01)**	**0.61 (SD 0.20)**

Table 2: Mean evaluation results for the similar patient retrieval task.

Method	SNOMED similarity score	Charlson Jaccard index
One hot encodings	4.40 (SD 2.32)	**0.88 (SD 0.30)**
Rocheteau's method[4]	3.52 (SD 3.26)	0.69 (SD 0.20)
Co-morbid patient embeddings	**1.78 (SD 1.90)**	0.84 (SD 0.34)

Table 3: Accuracy results for the case-based reasoning appropriate treatment task for the most common antibiotics (co-amoxiclav and ceftriaxone) and their classes (penecilins and cephalosporins).

Method	Antibiotic classification	Antibiotic class classification
Co-morbid patient embeddings	0.78	**0.79**
Rocheteau score	**0.80**	0.78
One hot encodings	0.75	0.75

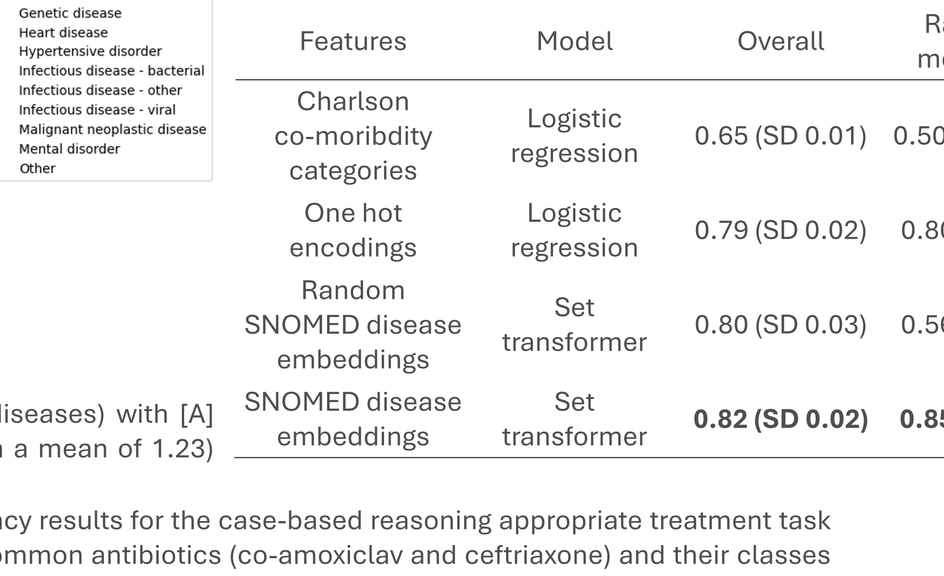

Figure 3: Proportion of human expert votes for patients identified by each method, for each question, in a survey. Co-morbid patient embeddings obtained the most votes for 6 questions.

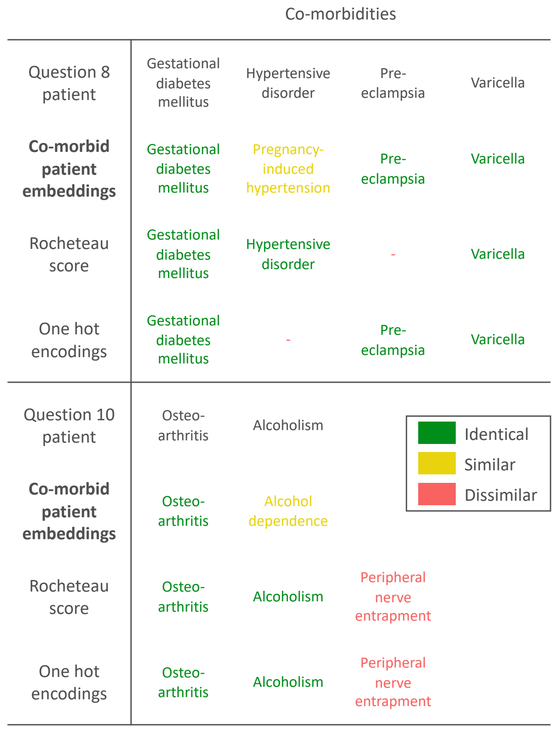

Figure 4: Two examples of the patient in question and the similar patients retrieved by each method. The similarity of co-morbidities is indicated through a traffic light coloring scheme.

Discussion

- We developed a **novel pipeline** to extract and utilize **untapped medical knowledge** and demonstrated its utility in classification, similar patient retrieval and antibiotic optimization tasks
- Our approach is **generalizable** and can overcome some problems with using disease data in AI systems as the **embeddings are not influenced by dataset size, the number of diseases or their rareness** and are **adaptable to variation in clinical documentation**
- Future work includes, considering **temporal** aspects and **embedding additional clinical data** such as demographics and medications

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